

EXHIBIT D

ClustalW (v1.4) multiple sequence alignment

5 Sequences Aligned Alignment Score = 707
Gaps Inserted = 20 Conserved Identities = 0

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
 Open Gap Penalty = 5.0 Extend Gap Penalty = 0.1
 Similarity Matrix: blosum

Multiple Alignment Parameters:
 Open Gap Penalty = 5.0 Extend Gap Penalty = 0.0
 Delay Divergent = 40% Gap Distance = 8
 Similarity Matrix: blosum

Processing time: 0.6 seconds

```
SEQ ID NO:5      1      MRLVLSSLLCILLLCFSIFSTEGKRRPAKAWSGRRT 37
AA283751-1      1  FGTREN-----LPSHHEASSPFQPALYP-ASLLLHLLHRREEASC----- 39
AA283751-2      1      SERGKICLLTMRLVLSSLLCILLLCFSIFSTEGKRRPANSL----- 42
AA283751-3      1      E-----SRPFIQRR---VML---S--RT----RELRSQ----- 21
AA283751-4      1  GWSL-----LGSLVDHS---ARY---VMCAQ-GSGAKATSP----- 29
```

```
SEQ ID NO:5      38  RLCCHRVSPNSTNLKGHHVRLCKPCKLEPEPRLWVVP GALPQV 81
AA283751-1      40  -----QQPGQAGEPGSAATESLAP-TQQT 62
AA283751-2      43  -----VRQENQALLPPSP 55
AA283751-3      22  -----IR-SRQKEM 29
AA283751-4      30  -----IG-CTYCELALS---WVASF---RM 47
```